

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: LABORATOIRES GOEMAR S.A.
- (B) STREET: La Madeleine B.P. 55
- (C) CITY: Saint-Malo
- (E) COUNTRY: France
- (F) POSTAL CODE (ZIP): 35413 Cedex
- (G) TELEPHONE: 99 21 53 70
- (H) TELEFAX: 99 82 56 17

(ii) TITLE OF INVENTION: Glycolyse hydrolase genes and their use for producing enzymes for the biodegradation of carrageenans

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2085 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(211..1683, 1880..2083)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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AAGCTTTCCG ATTCTATCAT CGAAGTCATA GGAGTGGGTA AACAAAAAAG CATGAAACTA      60
GCTTTTTTAAA ATACAGACTT TCAATATAGG TCGCACACAA TATTAACGAA TAAATAAGCA      120
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AATCATATAC ATAATCATTG CTTTAAATAT GTTTTAATAC AGATATAAAC ATAGTATGTT	180
TGTGTTTTTG GTATCTATCG GAGTGAAAAC ATG CGC TTA TAT TTT AGA AAG TTG	234
Met Arg Leu Tyr Phe Arg Lys Leu	
1 5	
TGG TTA ACA AAT TTA TTT TTA GGC GGA GCA CTG GCC TCT TCA GCT GCG	282
Trp Leu Thr Asn Leu Phe Leu Gly Gly Ala Leu Ala Ser Ser Ala Ala	
10 15 20	
ATA GGG GCT GTC TCC CCC AAG ACT TAT AAG GAC GCA GAT TTT TAT GTT	330
Ile Gly Ala Val Ser Pro Lys Thr Tyr Lys Asp Ala Asp Phe Tyr Val	
25 30 35 40	
GCC CCT ACT CAA CAA GAT GTT AAC TAT GAT TTA GTT GAT GAT TTT GGC	378
Ala Pro Thr Gln Gln Asp Val Asn Tyr Asp Leu Val Asp Asp Phe Gly	
45 50 55	
GCT AAT GGA AAC GAC ACT AGT GAT GAC AGT AAT GCT TTA CAA AGA GCA	426
Ala Asn Gly Asn Asp Thr Ser Asp Asp Ser Asn Ala Leu Gln Arg Ala	
60 65 70	
ATT AAT GCT ATT AGT AGA AAA CCG AAT GGG GGC ACT TTA CTA ATA CCG	474
Ile Asn Ala Ile Ser Arg Lys Pro Asn Gly Gly Thr Leu Leu Ile Pro	
75 80 85	
AAT GGA ACT TAC CAT TTC CTC GGC ATA CAG ATG AAG TCG AAC GTA CAC	522
Asn Gly Thr Tyr His Phe Leu Gly Ile Gln Met Lys Ser Asn Val His	
90 95 100	
ATC CGT GTT GAG AGT GAC GTG ATA ATC AAG CCA ACG TGG AAT GGG GAT	570
Ile Arg Val Glu Ser Asp Val Ile Ile Lys Pro Thr Trp Asn Gly Asp	
105 110 115 120	
GGC AAA AAC CAC CGA CTA TTT GAA GTT GGC GTA AAC AAT ATT GTA AGA	618
Gly Lys Asn His Arg Leu Phe Glu Val Gly Val Asn Asn Ile Val Arg	
125 130 135	
AAC TTC AGC TTT CAA GGG TTA GGA AAC GGT TTT TTG GTG GAT TTT AAA	666
Asn Phe Ser Phe Gln Gly Leu Gly Asn Gly Phe Leu Val Asp Phe Lys	
140 145 150	
GAT TCT CGC GAC AAA AAC TTA GCT GTT TTT AAG TTA GGC GAT GTT AGA	714
Asp Ser Arg Asp Lys Asn Leu Ala Val Phe Lys Leu Gly Asp Val Arg	
155 160 165	

AAT TAC AAA ATT TCC AAT TTT ACC ATT GAT GAT AAT AAA ACG ATA TTT Asn Tyr Lys Ile Ser Asn Phe Thr Ile Asp Asp Asn Lys Thr Ile Phe 170 175 180	762
GCC TCA ATT TTA GTG GAC GTA ACA GAA CGT AAT GGG CGG TTA CAT TGG Ala Ser Ile Leu Val Asp Val Thr Glu Arg Asn Gly Arg Leu His Trp 185 190 195 200	810
TCG CGT AAT GGA ATT ATC GAA AGA ATA AAA CAA AAT AAC GCT TTG TTC Ser Arg Asn Gly Ile Ile Glu Arg Ile Lys Gln Asn Asn Ala Leu Phe 205 210 215	858
GGC TAC GGC CTT ATT CAA ACC TAT GGC GCA GAT AAT ATT TTG TTT AGG Gly Tyr Gly Leu Ile Gln Thr Tyr Gly Ala Asp Asn Ile Leu Phe Arg 220 225 230	906
AAC CTC CAT TCG GAA GGC GGA ATT GCG TTA CGG ATG GAA ACT GAC AAC Asn Leu His Ser Glu Gly Gly Ile Ala Leu Arg Met Glu Thr Asp Asn 235 240 245	954
TTA CTT ATG AAA AAT TAT AAG CAA GGC GGA ATA AGA AAC ATC TTT GCT Leu Leu Met Lys Asn Tyr Lys Gln Gly Gly Ile Arg Asn Ile Phe Ala 250 255 260	1002
GAT AAT ATC AGA TGT AGC AAA GGA CTT GCG GCG GTC ATG TTT GGC CCA Asp Asn Ile Arg Cys Ser Lys Gly Leu Ala Ala Val Met Phe Gly Pro 265 270 275 280	1050
CAT TTT ATG AAG AAT GGA GAT GTG CAA GTG ACC AAT GTC AGC TCA GTT His Phe Met Lys Asn Gly Asp Val Gln Val Thr Asn Val Ser Ser Val 285 290 295	1098
AGT TGC GGT TCG GCT GTA CGA AGT GAT AGT GGA TTT GTC GAA CTC TTT Ser Cys Gly Ser Ala Val Arg Ser Asp Ser Gly Phe Val Glu Leu Phe 300 305 310	1146
AGC CCG ACA GAC GAA GTA CAT ACG CGT CAA AGT TGG AAA CAA GCC GTT Ser Pro Thr Asp Glu Val His Thr Arg Gln Ser Trp Lys Gln Ala Val 315 320 325	1194
GAA AGT AAA TTG GGC CGA GGG TGT GCG CAA ACC CCT TAT GCT AGA GGT Glu Ser Lys Leu Gly Arg Gly Cys Ala Gln Thr Pro Tyr Ala Arg Gly 330 335 340	1242

AAA AAT GCT CTT TTA TTT GCA GGC TTT TCG TTA AGT CTA GTT GCA CAG	1945
Lys Asn Ala Leu Leu Phe Ala Gly Phe Ser Leu Ser Leu Val Ala Gln	
500 505 510	
TCA GTT AGT GCA CAA GAA GCA AAA CAG CCT GAA AAA GAA GAA AAA GAT	1993
Ser Val Ser Ala Gln Glu Ala Lys Gln Pro Glu Lys Glu Glu Lys Asp	
515 520 525	
GTT GAG GTG ATT TTG GTA TCG GCA CAA AAG CGT GAG CAA GCG CTT AAA	2041
Val Glu Val Ile Leu Val Ser Ala Gln Lys Arg Glu Gln Ala Leu Lys	
530 535 540 545	
GAA GTG CCT GTA TCA ATT GAA GTT ATT CAA GGC GAC CTT CTA GA	2085
Glu Val Pro Val Ser Ile Glu Val Ile Gln Gly Asp Leu Leu	
550 555	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Arg Leu Tyr Phe Arg Lys Leu Trp Leu Thr Asn Leu Phe Leu Gly	
1 5 10 15	
Gly Ala Leu Ala Ser Ser Ala Ala Ile Gly Ala Val Ser Pro Lys Thr	
20 25 30	
Tyr Lys Asp Ala Asp Phe Tyr Val Ala Pro Thr Gln Gln Asp Val Asn	
35 40 45	
Tyr Asp Leu Val Asp Asp Phe Gly Ala Asn Gly Asn Asp Thr Ser Asp	
50 55 60	
Asp Ser Asn Ala Leu Gln Arg Ala Ile Asn Ala Ile Ser Arg Lys Pro	
65 70 75 80	
Asn Gly Gly Thr Leu Leu Ile Pro Asn Gly Thr Tyr His Phe Leu Gly	
85 90 95	
Ile Gln Met Lys Ser Asn Val His Ile Arg Val Glu Ser Asp Val Ile	
100 105 110	
Ile Lys Pro Thr Trp Asn Gly Asp Gly Lys Asn His Arg Leu Phe Glu	
115 120 125	
Val Gly Val Asn Asn Ile Val Arg Asn Phe Ser Phe Gln Gly Leu Gly	
130 135 140	

Asn Gly Phe Leu Val Asp Phe Lys Asp Ser Arg Asp Lys Asn Leu Ala															
145				150					155						160
Val Phe Lys Leu Gly Asp Val Arg Asn Tyr Lys Ile Ser Asn Phe Thr				165				170						175	
Ile Asp Asp Asn Lys Thr Ile Phe Ala Ser Ile Leu Val Asp Val Thr				180			185					190			
Glu Arg Asn Gly Arg Leu His Trp Ser Arg Asn Gly Ile Ile Glu Arg				195			200				205				
Ile Lys Gln Asn Asn Ala Leu Phe Gly Tyr Gly Leu Ile Gln Thr Tyr				210			215			220					
Gly Ala Asp Asn Ile Leu Phe Arg Asn Leu His Ser Glu Gly Gly Ile				225			230			235				240	
Ala Leu Arg Met Glu Thr Asp Asn Leu Leu Met Lys Asn Tyr Lys Gln				245				250						255	
Gly Gly Ile Arg Asn Ile Phe Ala Asp Asn Ile Arg Cys Ser Lys Gly				260			265					270			
Leu Ala Ala Val Met Phe Gly Pro His Phe Met Lys Asn Gly Asp Val				275			280					285			
Gln Val Thr Asn Val Ser Ser Val Ser Cys Gly Ser Ala Val Arg Ser				290			295				300				
Asp Ser Gly Phe Val Glu Leu Phe Ser Pro Thr Asp Glu Val His Thr				305			310			315				320	
Arg Gln Ser Trp Lys Gln Ala Val Glu Ser Lys Leu Gly Arg Gly Cys				325				330						335	
Ala Gln Thr Pro Tyr Ala Arg Gly Asn Gly Gly Thr Arg Trp Ala Ala				340			345					350			
Arg Val Thr Gln Lys Asp Ala Cys Leu Asp Lys Ala Lys Leu Glu Tyr				355			360					365			
Gly Ile Glu Pro Gly Ser Phe Gly Thr Val Lys Val Phe Asp Val Thr				370			375				380				
Ala Arg Phe Gly Tyr Asn Ala Asp Leu Lys Gln Asp Gln Leu Asp Tyr				385			390			395				400	
Phe Ser Thr Ser Asn Pro Met Cys Lys Arg Val Cys Leu Pro Thr Lys				405				410						415	
Glu Gln Trp Ser Lys Gln Gly Gln Ile Tyr Ile Gly Pro Ser Leu Ala				420			425							430	
Ala Val Ile Asp Thr Thr Pro Glu Thr Ser Lys Tyr Asp Tyr Asp Val				435			440					445			
Lys Thr Phe Asn Val Lys Arg Ile Asn Phe Pro Val Asn Ser His Lys				450			455				460				
Thr Ile Asp Thr Asn Thr Glu Ser Ser Arg Val Cys Asn Tyr Tyr Gly				465			470			475				480	
Met Ser Glu Cys Ser Ser Ser Arg Trp Glu Arg Met Lys Gly Val Ser				485				490						495	
Thr Lys Asn Ala Leu Leu Phe Ala Gly Phe Ser Leu Ser Leu Val Ala				500				505						510	

Gln Ser Val Ser Ala Gln Glu Ala Lys Gln Pro Glu Lys Glu Glu Lys
 515 520 525
 Asp Val Glu Val Ile Leu Val Ser Ala Gln Lys Arg Glu Gln Ala Leu
 530 535 540
 Lys Glu Val Pro Val Ser Ile Glu Val Ile Gln Gly Asp Leu Leu
 545 550 555

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1997 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(333..1805, 1866..1997)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCCTAAAAAC TATTCTTCAT ACCCTTTGAT GTATACGTTT AAACATATAGG GAGTTAATCT 60
 GGTTTTGGTG CAATTCTAGT TTAATAAATG AAGCCTTCTT TTTTGACTTA CATTTTATTA 120
 ACCTCTTGAA TTCTTGGGGC TTGCTAATTA TAAATACTT AATATCAGGT GGTGTGTGTA 180
 AAGAGGTGGA AGGGTATAGG ACCGTTACTT ATAATTGGCC CCTGTCGGAA GGGGGGTAA 240
 AGGTAAATA GTGTTTAAGT GTATTAATTA ACTTCTATAT AAGTAGGAAA ATACACTATA 300
 TATTGCGACA TTATTAACCT TAAATTCTTA CA ATG AAA TTA CAA TTT AAA CCT 353
 Met Lys Leu Gln Phe Lys Pro
 1 5

GTT TAT TTA GCG TCA ATT GCC ATA ATG GCA ATA GGA TGC ACC AAA GAA 401
 Val Tyr Leu Ala Ser Ile Ala Ile Met Ala Ile Gly Cys Thr Lys Glu
 10 15 20

GTG ACG GAA AAC GAT ACC TCC GAA ATT TCG GAA GTT CCA ACT GAA TTG 449
 Val Thr Glu Asn Asp Thr Ser Glu Ile Ser Glu Val Pro Thr Glu Leu
 25 30 35

AGG GCC GCG GCT TCT TCA TTT TAT ACC CCA CCG GGT CAG AAT GTA CGG 497
 Arg Ala Ala Ala Ser Ser Phe Tyr Thr Pro Pro Gly Gln Asn Val Arg
 40 45 50 55

GCC AAT AAA AAA AAC CTG GTC ACG GAT TAC GGT GTT AAC CAC AAT GAT	545
Ala Asn Lys Lys Asn Leu Val Thr Asp Tyr Gly Val Asn His Asn Asp	
60 65 70	
CAG AAC GAT GAT AGT AGC AAA TTA AAC CTG GCT ATC AAA GAT TTA TCG	593
Gln Asn Asp Asp Ser Ser Lys Leu Asn Leu Ala Ile Lys Asp Leu Ser	
75 80 85	
GAT ACC GGT GGT ATA CTG ACC CTT CCT AAG GGA AAG TAC TAT TTG ACC	641
Asp Thr Gly Gly Ile Leu Thr Leu Pro Lys Gly Lys Tyr Tyr Leu Thr	
90 95 100	
AAA ATT AGA ATG CGC TCT AAT GTA CAT CTT GAA ATA GAA AAG GGA ACG	689
Lys Ile Arg Met Arg Ser Asn Val His Leu Glu Ile Glu Lys Gly Thr	
105 110 115	
GTA ATC TAT CCG ACC AAG GGG TTG ACT CCT GCG AAG AAT CAC AGA ATT	737
Val Ile Tyr Pro Thr Lys Gly Leu Thr Pro Ala Lys Asn His Arg Ile	
120 125 130 135	
TTT GAT TTT GCC AGT AAA ACA GAG GAA AAA ATA GAA AAC GCC AGT ATA	785
Phe Asp Phe Ala Ser Lys Thr Glu Glu Lys Ile Glu Asn Ala Ser Ile	
140 145 150	
GTG GGT AAA GGA GGT AAG TTT ATA GTA GAC CTA AGA GGC AAC AGT TCT	833
Val Gly Lys Gly Gly Lys Phe Ile Val Asp Leu Arg Gly Asn Ser Ser	
155 160 165	
AAA AAC CAA ATT GTA GCC GAT GTT GGT AAC GTA ACC AAC TTT AAA ATA	881
Lys Asn Gln Ile Val Ala Asp Val Gly Asn Val Thr Asn Phe Lys Ile	
170 175 180	
TCG AAT TTT ACG ATC AAG GAT GAA AAA ACC ATC TTT GCT TCG ATA TTG	929
Ser Asn Phe Thr Ile Lys Asp Glu Lys Thr Ile Phe Ala Ser Ile Leu	
185 190 195	
GTA AGC TTT ACG GAT AAG GCA GGC AAT GCT TGG CCA CAT AAA GGT ATT	977
Val Ser Phe Thr Asp Lys Ala Gly Asn Ala Trp Pro His Lys Gly Ile	
200 205 210 215	
ATT GAG AAT ATA GAC CAG GCG AAT GCC CAT ACG GGA TAT GGC CTC ATA	1025
Ile Glu Asn Ile Asp Gln Ala Asn Ala His Thr Gly Tyr Gly Leu Ile	
220 225 230	

CAG GCG TAC GCG GCA GAT AAC ATT CTG TTC AAC AAT CTA AGT TGT ACG	1073
Gln Ala Tyr Ala Ala Asp Asn Ile Leu Phe Asn Asn Leu Ser Cys Thr	
235 240 245	
GGC GGG GTA ACC TTG CGT TTA GAA ACC GAC AAC CTC GCT ATG AAA ACC	1121
Gly Gly Val Thr Leu Arg Leu Glu Thr Asp Asn Leu Ala Met Lys Thr	
250 255 260	
GCT AAA AAA GGG GGG GTA AGG GAT ATT TTT GCC ACA AAG ATC AAG AAT	1169
Ala Lys Lys Gly Gly Val Arg Asp Ile Phe Ala Thr Lys Ile Lys Asn	
265 270 275	
ACC AAT GGC TTG ACC CCG GTA ATG TTC TCT CCC CAT TTT ATG GAA AAC	1217
Thr Asn Gly Leu Thr Pro Val Met Phe Ser Pro His Phe Met Glu Asn	
280 285 290 295	
GGT AAA GTG ACC ATA GAT GAT GTA ACC GCC ATC GGT TGT GCA TAT GCC	1265
Gly Lys Val Thr Ile Asp Asp Val Thr Ala Ile Gly Cys Ala Tyr Ala	
300 305 310	
GTA CGT GTA GAG CAC GGT TTT ATA GAG ATT TTC GAT AAG GGG AAT AGG	1313
Val Arg Val Glu His Gly Phe Ile Glu Ile Phe Asp Lys Gly Asn Arg	
315 320 325	
GCA AGT GCC GAC GCT TTC AAG AAC TAT ATT GAA GGT ATT CTA GGA GCT	1361
Ala Ser Ala Asp Ala Phe Lys Asn Tyr Ile Glu Gly Ile Leu Gly Ala	
330 335 340	
GGC TCG GTA GAA GTC GTG TAC AAA CGT AAT AAC GGA AGA ACA TGG GCG	1409
Gly Ser Val Glu Val Val Tyr Lys Arg Asn Asn Gly Arg Thr Trp Ala	
345 350 355	
GCA CGT ATC GCA AAC GAC TTT AAC GAA GCG GCG TAT AAC CAC TCC AAT	1457
Ala Arg Ile Ala Asn Asp Phe Asn Glu Ala Ala Tyr Asn His Ser Asn	
360 365 370 375	
CCT GCC GTT AGC GGA ATC AAA CCA GGG AAA TTC GCC ACA TCT AAG GTA	1505
Pro Ala Val Ser Gly Ile Lys Pro Gly Lys Phe Ala Thr Ser Lys Val	
380 385 390	
ACC AAT GTT AAG GCA ACC TAT AAG GGT ACT GGC GCC AAA CTC AAG CAG	1553
Thr Asn Val Lys Ala Thr Tyr Lys Gly Thr Gly Ala Lys Leu Lys Gln	
395 400 405	

GCA TTC TTA TCC TAT TTA CCC TGT TCG GAA CGT TCT AAG GTT TGT CGG	1601
Ala Phe Leu Ser Tyr Leu Pro Cys Ser Glu Arg Ser Lys Val Cys Arg	
410 415 420	
CCA GGT CCA GAT GGG TTC GAG TAT AAC GGA CCC TCC TTG GGA GTT ACC	1649
Pro Gly Pro Asp Gly Phe Glu Tyr Asn Gly Pro Ser Leu Gly Val Thr	
425 430 435	
ATC GAT AAC ACG AAA AGG GAC AAC AGC CTT GGC AAT TAT AAC GTC AAT	1697
Ile Asp Asn Thr Lys Arg Asp Asn Ser Leu Gly Asn Tyr Asn Val Asn	
440 445 450 455	
GTA AGC ACC TCC AGT GTT CAG GGC TTT CCC AAT AAT TAC GTT TTA AAC	1745
Val Ser Thr Ser Ser Val Gln Gly Phe Pro Asn Asn Tyr Val Leu Asn	
460 465 470	
GTA AAG TAT AAT ACC CCT AAA GTA TGT AAC CAA AAT CTA GGT AGT ATT	1793
Val Lys Tyr Asn Thr Pro Lys Val Cys Asn Gln Asn Leu Gly Ser Ile	
475 480 485	
ACT TCG TGT AAC TGATCACGAA ACAATTTGTA AATAAAAAGC AGCTGTCCCT	1845
Thr Ser Cys Asn	
490	
TATTACGGGC GGCTGCTTTT ATG TCT TTA AGC CAT GTC GTG ATT TAT TGG	1895
Met Ser Leu Ser His Val Val Ile Tyr Trp	
495 500	
CGA CTT TTG ATA AAG GCT TGG ATT TCT TCC GGG GTA AAT ATC GGA TTG	1943
Arg Leu Leu Ile Lys Ala Trp Ile Ser Ser Gly Val Asn Ile Gly Leu	
505 510 515	
GCC CCT TCC CTA CCG GCT ACC ATA GCT CTA TGC TCC TAT GCA CAG GCG	1991
Ala Pro Ser Leu Pro Ala Thr Ile Ala Leu Cys Ser Tyr Ala Gln Ala	
520 525 530	
AAA TCT	1997
Lys Ser	
535	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Lys	Leu	Gln	Phe	Lys	Pro	Val	Tyr	Leu	Ala	Ser	Ile	Ala	Ile	Met
1				5					10					15	
Ala	Ile	Gly	Cys	Thr	Lys	Glu	Val	Thr	Glu	Asn	Asp	Thr	Ser	Glu	Ile
		20						25					30		
Ser	Glu	Val	Pro	Thr	Glu	Leu	Arg	Ala	Ala	Ala	Ser	Ser	Phe	Tyr	Thr
		35					40					45			
Pro	Pro	Gly	Gln	Asn	Val	Arg	Ala	Asn	Lys	Lys	Asn	Leu	Val	Thr	Asp
		50				55					60				
Tyr	Gly	Val	Asn	His	Asn	Asp	Gln	Asn	Asp	Asp	Ser	Ser	Lys	Leu	Asn
		65			70				75					80	
Leu	Ala	Ile	Lys	Asp	Leu	Ser	Asp	Thr	Gly	Gly	Ile	Leu	Thr	Leu	Pro
			85						90					95	
Lys	Gly	Lys	Tyr	Tyr	Leu	Thr	Lys	Ile	Arg	Met	Arg	Ser	Asn	Val	His
			100					105					110		
Leu	Glu	Ile	Glu	Lys	Gly	Thr	Val	Ile	Tyr	Pro	Thr	Lys	Gly	Leu	Thr
		115					120					125			
Pro	Ala	Lys	Asn	His	Arg	Ile	Phe	Asp	Phe	Ala	Ser	Lys	Thr	Glu	Glu
		130				135					140				
Lys	Ile	Glu	Asn	Ala	Ser	Ile	Val	Gly	Lys	Gly	Gly	Lys	Phe	Ile	Val
		145			150				155					160	
Asp	Leu	Arg	Gly	Asn	Ser	Ser	Lys	Asn	Gln	Ile	Val	Ala	Asp	Val	Gly
			165					170					175		
Asn	Val	Thr	Asn	Phe	Lys	Ile	Ser	Asn	Phe	Thr	Ile	Lys	Asp	Glu	Lys
		180						185					190		
Thr	Ile	Phe	Ala	Ser	Ile	Leu	Val	Ser	Phe	Thr	Asp	Lys	Ala	Gly	Asn
		195				200						205			
Ala	Trp	Pro	His	Lys	Gly	Ile	Ile	Glu	Asn	Ile	Asp	Gln	Ala	Asn	Ala
		210				215					220				
His	Thr	Gly	Tyr	Gly	Leu	Ile	Gln	Ala	Tyr	Ala	Ala	Asp	Asn	Ile	Leu
		225			230				235					240	
Phe	Asn	Asn	Leu	Ser	Cys	Thr	Gly	Gly	Val	Thr	Leu	Arg	Leu	Glu	Thr
			245					250						255	
Asp	Asn	Leu	Ala	Met	Lys	Thr	Ala	Lys	Lys	Gly	Gly	Val	Arg	Asp	Ile
		260						265					270		
Phe	Ala	Thr	Lys	Ile	Lys	Asn	Thr	Asn	Gly	Leu	Thr	Pro	Val	Met	Phe
		275				280						285			
Ser	Pro	His	Phe	Met	Glu	Asn	Gly	Lys	Val	Thr	Ile	Asp	Asp	Val	Thr
		290				295					300				
Ala	Ile	Gly	Cys	Ala	Tyr	Ala	Val	Arg	Val	Glu	His	Gly	Phe	Ile	Glu
		305			310					315				320	

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Ile Phe Asp Lys Gly Asn Arg Ala Ser Ala Asp Ala Phe Lys Asn Tyr
      325                      330                      335
Ile Glu Gly Ile Leu Gly Ala Gly Ser Val Glu Val Val Tyr Lys Arg
      340                      345                      350
Asn Asn Gly Arg Thr Trp Ala Ala Arg Ile Ala Asn Asp Phe Asn Glu
      355                      360                      365
Ala Ala Tyr Asn His Ser Asn Pro Ala Val Ser Gly Ile Lys Pro Gly
      370                      375                      380
Lys Phe Ala Thr Ser Lys Val Thr Asn Val Lys Ala Thr Tyr Lys Gly
385                      390                      395                      400
Thr Gly Ala Lys Leu Lys Gln Ala Phe Leu Ser Tyr Leu Pro Cys Ser
      405                      410                      415
Glu Arg Ser Lys Val Cys Arg Pro Gly Pro Asp Gly Phe Glu Tyr Asn
      420                      425                      430
Gly Pro Ser Leu Gly Val Thr Ile Asp Asn Thr Lys Arg Asp Asn Ser
      435                      440                      445
Leu Gly Asn Tyr Asn Val Asn Val Ser Thr Ser Ser Val Gln Gly Phe
450                      455                      460
Pro Asn Asn Tyr Val Leu Asn Val Lys Tyr Asn Thr Pro Lys Val Cys
465                      470                      475                      480
Asn Gln Asn Leu Gly Ser Ile Thr Ser Cys Asn Met Ser Leu Ser His
      485                      490                      495
Val Val Ile Tyr Trp Arg Leu Leu Ile Lys Ala Trp Ile Ser Ser Gly
      500                      505                      510
Val Asn Ile Gly Leu Ala Pro Ser Leu Pro Ala Thr Ile Ala Leu Cys
      515                      520                      525
Ser Tyr Ala Gln Ala Lys Ser
      530                      535

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1..498, 741..1931, 2009..2179)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GAT CAT ATC ATT CCT TTG CAA ATT AAA AAT TCT CAA GAT AGT CAA ATA	48
Asp His Ile Ile Pro Leu Gln Ile Lys Asn Ser Gln Asp Ser Gln Ile	
1 5 10 15	
ATT AGT TTT TTT AAA GCT GAC AAA GGG AGT GTG AGC AGG CAA GTA CAC	96
Ile Ser Phe Phe Lys Ala Asp Lys Gly Ser Val Ser Arg Gln Val His	
20 25 30	
CCA CCT TGG CCT GTG CCT TGT AAA AGT AAA CTG CAA GAG CAA GAT AGT	144
Pro Pro Trp Pro Val Pro Cys Lys Ser Lys Leu Gln Glu Gln Asp Ser	
35 40 45	
AGT GAG TCT AAA GAG AGT AAG GCA GAG CAA GTT AAA ATT AAC AAC TGC	192
Ser Glu Ser Lys Glu Ser Lys Ala Glu Gln Val Lys Ile Asn Asn Cys	
50 55 60	
GTT GTA CAG AAC GCA ATG CTG TAC ATA GAA AAC AAT TAT TTC AAC GAT	240
Val Val Gln Asn Ala Met Leu Tyr Ile Glu Asn Asn Tyr Phe Asn Asp	
65 70 75 80	
ATA AAT ATA GAC ACG GTT GCT TTT TCT GTT GGC GTA AGT CGC TCT TAT	288
Ile Asn Ile Asp Thr Val Ala Phe Ser Val Gly Val Ser Arg Ser Tyr	
85 90 95	
CTC GTT AAA CAA TTT AAG TTA GCA ACG AAT AAA ACG ATT AAT AAT AGA	336
Leu Val Lys Gln Phe Lys Leu Ala Thr Asn Lys Thr Ile Asn Asn Arg	
100 105 110	
ATC ATA GAA GTA AGA ATA GAG CAG GCT AAA AAA GTA TTA CTA AAA AAA	384
Ile Ile Glu Val Arg Ile Glu Gln Ala Lys Lys Val Leu Leu Lys Lys	
115 120 125	
TCT GTT ACA GAA ACA GCT TAT GAA GTT GGT TTT AAT AAC TCA AAC TAC	432
Ser Val Thr Glu Thr Ala Tyr Glu Val Gly Phe Asn Asn Ser Asn Tyr	
130 135 140	
TTC GCG ACA GTT TTT AAA AAA AGA ACA AAC TAC ACG CCC AAG CAA TTT	480
Phe Ala Thr Val Phe Lys Lys Arg Thr Asn Tyr Thr Pro Lys Gln Phe	
145 150 155 160	
AAA CGT ACT TTT TCC AGC TAAACTACA ACTAAATAAC GATTAAAAGC	528
Lys Arg Thr Phe Ser Ser	
165	
CATTTT TAGA GAACAGTAAA ACCATTTTTT GAGGTTTGGT GTTGATATATA AATATTAAAT	588

ATCCCCACTC GCTCAGCTTT TTTTGTGCGA GTTGTGAGAA TTAGCTTAAC AGGTAAGGTT	648
TACGTATCTG TATATCTAAA CTCTTCGAAT ATAACACTGT ATCTGTTGCT GAGCTGTGGC	708
TCAGTTCACA CTAACAAAGG ATGGATAAAT AA ATG AAA CCT ATA AGT ATT GTG	761
Met Lys Pro Ile Ser Ile Val	
170	
GCA TTC CCT ATA CCA GCT ATA AGT ATG CTT CTT TTA AGT GCA GTA TCA	809
Ala Phe Pro Ile Pro Ala Ile Ser Met Leu Leu Leu Ser Ala Val Ser	
175 180 185	
CAA GCA GCA TCT ATG CAA CCT CCC ATC GCA AAA CCT GGT GAA ACA TGG	857
Gln Ala Ala Ser Met Gln Pro Pro Ile Ala Lys Pro Gly Glu Thr Trp	
190 195 200 205	
ATT TTA CAA GCC AAA CGC TCT GAC GAA TTT AAC GTA AAA GAT GCG ACA	905
Ile Leu Gln Ala Lys Arg Ser Asp Glu Phe Asn Val Lys Asp Ala Thr	
210 215 220	
AAG TGG AAC TTT CAA ACA GAA AAC TAT GGG GTA TGG TCT TGG AAA AAT	953
Lys Trp Asn Phe Gln Thr Glu Asn Tyr Gly Val Trp Ser Trp Lys Asn	
225 230 235	
GAA AAT GCG ACA GTA TCT AAT GGC AAA CTA AAA TTA ACC ACT AAG CGA	1001
Glu Asn Ala Thr Val Ser Asn Gly Lys Leu Lys Leu Thr Thr Lys Arg	
240 245 250	
GAA TCT CAT CAA CGT ACA TTC TGG GAT GGC TGT AAT CAG CAG CAA GTT	1049
Glu Ser His Gln Arg Thr Phe Trp Asp Gly Cys Asn Gln Gln Gln Val	
255 260 265	
GCA AAT TAC CCA CTT TAT TAT ACA TCG GGT GTC GCT AAA TCC AGA GCT	1097
Ala Asn Tyr Pro Leu Tyr Tyr Thr Ser Gly Val Ala Lys Ser Arg Ala	
270 275 280 285	
ACA GGT AAT TAT GGC TAT TAC GAA GCT CGA ATC AAA GGA GCG AGT ACA	1145
Thr Gly Asn Tyr Gly Tyr Tyr Glu Ala Arg Ile Lys Gly Ala Ser Thr	
290 295 300	
TTT CCT GGC GTA TCG CCT GCT TTT TGG ATG TAT AGC ACC ATT GAC CGT	1193
Phe Pro Gly Val Ser Pro Ala Phe Trp Met Tyr Ser Thr Ile Asp Arg	
305 310 315	
TCA TTA ACG AAA GAA GGG GAT GTC CAA TAT AGC GAA ATA GAC GTA GTG	1241
Ser Leu Thr Lys Glu Gly Asp Val Gln Tyr Ser Glu Ile Asp Val Val	
320 325 330	

GAA CTT ACT CAA AAA AGT GCA GTG AGA GAG TCT GAT CAT GAC TTA CAC	1289
Glu Leu Thr Gln Lys Ser Ala Val Arg Glu Ser Asp His Asp Leu His	
335 340 345	
AAT ATT GTA GTA AAA AAT GGA AAA CCA ACA TGG ATG CGT CCA GGG TCT	1337
Asn Ile Val Val Lys Asn Gly Lys Pro Thr Trp Met Arg Pro Gly Ser	
350 355 360 365	
TTT CCG CAG ACA AAT CAT AAC GGA TAC CAT CTA CCT TTC GAT CCT CGA	1385
Phe Pro Gln Thr Asn His Asn Gly Tyr His Leu Pro Phe Asp Pro Arg	
370 375 380	
AAT GAC TTT CAC ACC TAT GGT GTC AAT GTA ACT AAA GAC AAG ATC ACT	1433
Asn Asp Phe His Thr Tyr Gly Val Asn Val Thr Lys Asp Lys Ile Thr	
385 390 395	
TGG TAC GTA GAT GGT GAA ATT GTG GGC GAA AAG GAT AAC TTA TAC TGG	1481
Trp Tyr Val Asp Gly Glu Ile Val Gly Glu Lys Asp Asn Leu Tyr Trp	
400 405 410	
CAT CGT CAA ATG AAT CTC ACA TTA TCA CAA GGC TTA CGC GCG CCG CAT	1529
His Arg Gln Met Asn Leu Thr Leu Ser Gln Gly Leu Arg Ala Pro His	
415 420 425	
ACA CAA TGG AAA TGT AAT CAA TTT TAC CCA TCA GCG AAT AAA TCA GCA	1577
Thr Gln Trp Lys Cys Asn Gln Phe Tyr Pro Ser Ala Asn Lys Ser Ala	
430 435 440 445	
GAA GGC TTC CCA ACA TCA ATG GAA GTT GAT TAT GTA AGA ACG TGG GTA	1625
Glu Gly Phe Pro Thr Ser Met Glu Val Asp Tyr Val Arg Thr Trp Val	
450 455 460	
AAG GTG GGC AAT AAC AAC TCT GCT CCA GGC GAG GGG CAG TCA TGT CCT	1673
Lys Val Gly Asn Asn Asn Ser Ala Pro Gly Glu Gly Gln Ser Cys Pro	
465 470 475	
AAC ACG TTT GTA GCT GTC AAT AGT GTT CAA CTA AGC GCA GCA AAA CAA	1721
Asn Thr Phe Val Ala Val Asn Ser Val Gln Leu Ser Ala Ala Lys Gln	
480 485 490	
ACA CTT CGA AAG GGC CAA TCT ACA ACG CTA GAA AGC ACA GTT CTT CCA	1769
Thr Leu Arg Lys Gly Gln Ser Thr Thr Leu Glu Ser Thr Val Leu Pro	
495 500 505	

TCA AAA GGA AAG CTT GAT C 2180
Ser Lys Gly Lys Leu Asp
615 620

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp	His	Ile	Ile	Pro	Leu	Gln	Ile	Lys	Asn	Ser	Gln	Asp	Ser	Gln	Ile
1				5				10						15	
Ile	Ser	Phe	Phe	Lys	Ala	Asp	Lys	Gly	Ser	Val	Ser	Arg	Gln	Val	His
			20					25					30		
Pro	Pro	Trp	Pro	Val	Pro	Cys	Lys	Ser	Lys	Leu	Gln	Glu	Gln	Asp	Ser
		35					40					45			
Ser	Glu	Ser	Lys	Glu	Ser	Lys	Ala	Glu	Gln	Val	Lys	Ile	Asn	Asn	Cys
	50					55					60				
Val	Val	Gln	Asn	Ala	Met	Leu	Tyr	Ile	Glu	Asn	Asn	Tyr	Phe	Asn	Asp
65					70					75					80
Ile	Asn	Ile	Asp	Thr	Val	Ala	Phe	Ser	Val	Gly	Val	Ser	Arg	Ser	Tyr
			85						90					95	
Leu	Val	Lys	Gln	Phe	Lys	Leu	Ala	Thr	Asn	Lys	Thr	Ile	Asn	Asn	Arg
			100					105					110		
Ile	Ile	Glu	Val	Arg	Ile	Glu	Gln	Ala	Lys	Lys	Val	Leu	Leu	Lys	Lys
		115					120					125			
Ser	Val	Thr	Glu	Thr	Ala	Tyr	Glu	Val	Gly	Phe	Asn	Asn	Ser	Asn	Tyr
	130					135					140				
Phe	Ala	Thr	Val	Phe	Lys	Lys	Arg	Thr	Asn	Tyr	Thr	Pro	Lys	Gln	Phe
145					150					155					160
Lys	Arg	Thr	Phe	Ser	Met	Lys	Pro	Ile	Ser	Ile	Val	Ala	Phe	Pro	
			165					170					175		
Ile	Pro	Ala	Ile	Ser	Met	Leu	Leu	Leu	Ser	Ala	Val	Ser	Gln	Ala	Ala
			180					185					190		
Ser	Met	Gln	Pro	Pro	Ile	Ala	Lys	Pro	Gly	Glu	Thr	Trp	Ile	Leu	Gln
		195					200					205			
Ala	Lys	Arg	Ser	Asp	Glu	Phe	Asn	Val	Lys	Asp	Ala	Thr	Lys	Trp	Asn
	210					215					220				
Phe	Gln	Thr	Glu	Asn	Tyr	Gly	Val	Trp	Ser	Trp	Lys	Asn	Glu	Asn	Ala
225					230					235					240
Thr	Val	Ser	Asn	Gly	Lys	Leu	Lys	Leu	Thr	Thr	Lys	Arg	Glu	Ser	His
			245						250					255	
Gln	Arg	Thr	Phe	Trp	Asp	Gly	Cys	Asn	Gln	Gln	Gln	Val	Ala	Asn	Tyr
		260					265						270		
Pro	Leu	Tyr	Tyr	Thr	Ser	Gly	Val	Ala	Lys	Ser	Arg	Ala	Thr	Gly	Asn
		275					280					285			
Tyr	Gly	Tyr	Tyr	Glu	Ala	Arg	Ile	Lys	Gly	Ala	Ser	Thr	Phe	Pro	Gly
	290					295					300				
Val	Ser	Pro	Ala	Phe	Trp	Met	Tyr	Ser	Thr	Ile	Asp	Arg	Ser	Leu	Thr
305					310					315					320
Lys	Glu	Gly	Asp	Val	Gln	Tyr	Ser	Glu	Ile	Asp	Val	Val	Glu	Leu	Thr
			325						330					335	
Gln	Lys	Ser	Ala	Val	Arg	Glu	Ser	Asp	His	Asp	Leu	His	Asn	Ile	Val
			340					345					350		

Val	Lys	Asn	Gly	Lys	Pro	Thr	Trp	Met	Arg	Pro	Gly	Ser	Phe	Pro	Gln
		355					360					365			
Thr	Asn	His	Asn	Gly	Tyr	His	Leu	Pro	Phe	Asp	Pro	Arg	Asn	Asp	Phe
		370				375					380				
His	Thr	Tyr	Gly	Val	Asn	Val	Thr	Lys	Asp	Lys	Ile	Thr	Trp	Tyr	Val
385					390					395					400
Asp	Gly	Glu	Ile	Val	Gly	Glu	Lys	Asp	Asn	Leu	Tyr	Trp	His	Arg	Gln
				405					410					415	
Met	Asn	Leu	Thr	Leu	Ser	Gln	Gly	Leu	Arg	Ala	Pro	His	Thr	Gln	Trp
			420					425					430		
Lys	Cys	Asn	Gln	Phe	Tyr	Pro	Ser	Ala	Asn	Lys	Ser	Ala	Glu	Gly	Phe
		435					440					445			
Pro	Thr	Ser	Met	Glu	Val	Asp	Tyr	Val	Arg	Thr	Trp	Val	Lys	Val	Gly
		450				455					460				
Asn	Asn	Asn	Ser	Ala	Pro	Gly	Glu	Gly	Gln	Ser	Cys	Pro	Asn	Thr	Phe
465					470					475					480
Val	Ala	Val	Asn	Ser	Val	Gln	Leu	Ser	Ala	Ala	Lys	Gln	Thr	Leu	Arg
				485					490					495	
Lys	Gly	Gln	Ser	Thr	Thr	Leu	Glu	Ser	Thr	Val	Leu	Pro	Asn	Cys	Ala
			500					505					510		
Thr	Asn	Lys	Lys	Val	Ile	Tyr	Ser	Ser	Ser	Asn	Lys	Asn	Val	Ala	Thr
		515				520						525			
Val	Asn	Ser	Ala	Gly	Val	Val	Lys	Ala	Lys	Asn	Lys	Gly	Thr	Ala	Thr
		530				535					540				
Ile	Thr	Val	Lys	Thr	Lys	Asn	Lys	Gly	Lys	Ile	Asp	Lys	Leu	Thr	Ile
545					550					555					560
Ala	Val	Asn	Met	Lys	Lys	Val	Asn	Leu	Ser	Ser	Lys	Trp	Ile	Ile	Ser
				565					570					575	
Ile	Ser	Leu	Leu	Ile	Ile	Cys	Asp	Tyr	Val	Tyr	Leu	Ile	Arg	Thr	Asn
			580					585					590		
Val	Asn	Glu	Gln	Ala	Asn	Ala	Glu	Ala	Thr	Ala	His	Met	His	Tyr	Lys
		595					600					605			
Ile	Asn	Asn	Thr	Lys	His	Ser	Lys	Gly	Lys	Leu	Asp				
	610					615					620				

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 875..2509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCCTCCGTAT TCGACAATGT TGTACGATGC TTGGCGATTC GGACTCTGTT TAAGCACTCG	60
ATTTTCGTAAA GGCACATATCC ACTCATTCAT TCCGACTCAA TATTCTTTTC GACAAATGCA	120
ACCGGTTCCA TTGAAAAGGC CCTAAAAATA CAGCTTTCCC GCCCCCATC GTAGAAGGTT	180
CCAATATGCT TCAACCCCTT TTTCAGCCTT ACTTCAGGGG TATTACTTTC ATGCCTAGGG	240
CCGCAAATAC ATTCGCTTGG ACCCAGTCAC CTATATAATT GAATACGGAA CTACCCATGG	300
CTTCCTTCCC TTTGGGAACC TATGGTACAG ACTTGCCTTT TTAAACCGG TTAATTTCAGC	360
TAATTCGCCA AGCTGGTTCC TTCATAACCT TTGGCCCGAA ACACCTTGCA AGCACATAAA	420
TCTTATCCAA TATTTTGCGG TCTCATGGGA CAAATCTATA ACAAACATTC AATTTTACCA	480
AACGTTCCGGT AATAAATCTA GTCAAAAACG GGGTCCGATT CATTTTAGAA GAAAGGTAAA	540
GCCCCCAAAA GAGCGGTTTA CTTGAAGATA TGATTTATAA AACACAATAA GTGACAAAGG	600
AAGATCATGG CTATAATTAG TTGAAAAAAC AGGGCTTACC ATGACATGGA GCTTTATTGA	660
AAACAGATGT CCAACAAGAA TAAAGGAGGG CCGTTCGACC GCGACGTTTA AATAAAAAACA	720
TATTCATAT CAAAATTTAA TTAAGGTTCT TTCCTACAGT ATTTATAAGA AATTACTAAA	780
ATTAGTTAGG ATAATACTAC AAAATGGTAA AATTGGATTA CTCAGATTGA ACCATAGCCT	840
CTACTTTAGT CGGCTAACAA AAACAATTAT AGTA ATG AAA AAA CCA AAT TTT	892
Met Lys Lys Pro Asn Phe	
1 5	
TAT GGC AAG ATG GGT AGA ACT GCA CTT TCA AGT CTT TTC TAC CTC TTT	940
Tyr Gly Lys Met Gly Arg Thr Ala Leu Ser Ser Leu Phe Tyr Leu Phe	
10 15 20	
TTC CTA GGC CTT GTG TAT GGG CAA CAA CCT ACG AAG ACT TCA AAT CCG	988
Phe Leu Gly Leu Val Tyr Gly Gln Gln Pro Thr Lys Thr Ser Asn Pro	
25 30 35	
AAC GAT CAG TGG ACC ATC AAA TGG AGT GCT TCG GAC GAA TTC AAC AAA	1036
Asn Asp Gln Trp Thr Ile Lys Trp Ser Ala Ser Asp Glu Phe Asn Lys	
40 45 50	
AAT GAC CCC GAC TGG GCA AAA TGG ATC AAG ACA GGA AAC CTT CCG AAT	1084
Asn Asp Pro Asp Trp Ala Lys Trp Ile Lys Thr Gly Asn Leu Pro Asn	
55 60 65 70	
ACA TCG GCA TGG AAA TGG AAC AAT CAA AAA AAC GTA AAG ATT TCC AAC	1132
Thr Ser Ala Trp Lys Trp Asn Asn Gln Lys Asn Val Lys Ile Ser Asn	
75 80 85	

GGA ATT GCG GAA CTA ACG ATG AGG CAT AAC GCC AAT AAT ACC CCA CCT	1180
Gly Ile Ala Glu Leu Thr Met Arg His Asn Ala Asn Asn Thr Pro Pro	
90 95 100	
GAC GGA GGA ACC TAT TTC ACC TCT GGG ATA TTT AAG TCG TAC CAA AAA	1228
Asp Gly Gly Thr Tyr Phe Thr Ser Gly Ile Phe Lys Ser Tyr Gln Lys	
105 110 115	
TTT ACG TAT GGA TAC TTT GAG GCC AAA ATC CAA GGA GCG GAT ATA GGT	1276
Phe Thr Tyr Gly Tyr Phe Glu Ala Lys Ile Gln Gly Ala Asp Ile Gly	
120 125 130	
GAA GGC GTA TGC CCA TCG TTT TGG CTT TAT AGT GAT TTC GAC TAT TCC	1324
Glu Gly Val Cys Pro Ser Phe Trp Leu Tyr Ser Asp Phe Asp Tyr Ser	
135 140 145 150	
GTA GCC AAT GGG GAA ACG GTA TAC AGT GAA ATA GAT GTA GTT GAA CTA	1372
Val Ala Asn Gly Glu Thr Val Tyr Ser Glu Ile Asp Val Val Glu Leu	
155 160 165	
CAA CAA TTC GAT TGG TAT GAA GGC CAT CAG GAC GAC ATT TAC GAC ATG	1420
Gln Gln Phe Asp Trp Tyr Glu Gly His Gln Asp Asp Ile Tyr Asp Met	
170 175 180	
GAC TTA AAT CTA CAC GCC GTT GTC AAA GAA AAC GGA CAG GGG GTT TGG	1468
Asp Leu Asn Leu His Ala Val Val Lys Glu Asn Gly Gln Gly Val Trp	
185 190 195	
AAA AGG CCA AAA ATG TAC CCT CAA GAA CAG TTG AAC AAA TGG AGA GCC	1516
Lys Arg Pro Lys Met Tyr Pro Gln Glu Gln Leu Asn Lys Trp Arg Ala	
200 205 210	
ATG GAC CCG AGT AAA GAC TTT CAT ATC TAT GGT TGT GAA GTG AAC CAG	1564
Met Asp Pro Ser Lys Asp Phe His Ile Tyr Gly Cys Glu Val Asn Gln	
215 220 225 230	
AAC GAA ATC ATA TGG TAT GTT GAC GGT GTC GAG GTT GCC CGA AAA CCA	1612
Asn Glu Ile Ile Trp Tyr Val Asp Gly Val Glu Val Ala Arg Lys Pro	
235 240 245	
AAT AAA TAT TGG CAT CGC CCC ATG AAC GTT ACC CTT TCA TTG GGA CTC	1660
Asn Lys Tyr Trp His Arg Pro Met Asn Val Thr Leu Ser Leu Gly Leu	
250 255 260	

AGA AAA CCA TTT GTG AAA TTT TTC GAC AAT AAG AAC AAT GCC ATA AAT	1708
Arg Lys Pro Phe Val Lys Phe Phe Asp Asn Lys Asn Asn Ala Ile Asn	
265 270 275	
CCA GAA ACC GAT GCC AAG GCA AGG GAA AAA TTA TCG GAT ATA CCT ACA	1756
Pro Glu Thr Asp Ala Lys Ala Arg Glu Lys Leu Ser Asp Ile Pro Thr	
280 285 290	
TCG ATG TAT GTG GAT TAC GTT CGG GTC TGG GAA AAA TCA GCA GGT AAC	1804
Ser Met Tyr Val Asp Tyr Val Arg Val Trp Glu Lys Ser Ala Gly Asn	
295 300 305 310	
ACT ACC AAT CCC CCA ACC AGC GAG GTC GGC ACA CTA AAA ACA AAG GGT	1852
Thr Thr Asn Pro Pro Thr Ser Glu Val Gly Thr Leu Lys Thr Lys Gly	
315 320 325	
TCG AAA CTG GTG ATT GAC CAT TGG GAT GCA AGT ACA GGG ACT ATT TCG	1900
Ser Lys Leu Val Ile Asp His Trp Asp Ala Ser Thr Gly Thr Ile Ser	
330 335 340	
GCT GTC AGT AAC AAT ACA AAG ACA GGT CAA TAT GCC GGT TCA GTG AAC	1948
Ala Val Ser Asn Asn Thr Lys Thr Gly Gln Tyr Ala Gly Ser Val Asn	
345 350 355	
AAC GCG AGC ATC GCC CAG ATA GTA ACA TTA AAA GCG AAT ACT TCA TAT	1996
Asn Ala Ser Ile Ala Gln Ile Val Thr Leu Lys Ala Asn Thr Ser Tyr	
360 365 370	
AAG GTA TCG GCT TTC GGA AAG GCC AGC TCA CCC GGA ACA TCG GCT TAT	2044
Lys Val Ser Ala Phe Gly Lys Ala Ser Ser Pro Gly Thr Ser Ala Tyr	
375 380 385 390	
CTA GGC ATT AGT AAA GCA TCC AAC AAC GAA CTC ATA AGC AAT TTT GAA	2092
Leu Gly Ile Ser Lys Ala Ser Asn Asn Glu Leu Ile Ser Asn Phe Glu	
395 400 405	
TTC AAA ACA ACC TCA TAC TCC AAA GGC GAG ATT GAG ATA AGA ACT GGA	2140
Phe Lys Thr Thr Ser Tyr Ser Lys Gly Glu Ile Glu Ile Arg Thr Gly	
410 415 420	
AAT GTT CAG GAA TCA TAT CGC ATA TGG TAT TGG TCT TCC GGG CAA GCC	2188
Asn Val Gln Glu Ser Tyr Arg Ile Trp Tyr Trp Ser Ser Gly Gln Ala	
425 430 435	

TAT TGC GAT GAT TTT AAC CTT GTT GAA ATA AAC AGC GGG GCT TCA CAA	2236
Tyr Cys Asp Asp Phe Asn Leu Val Glu Ile Asn Ser Gly Ala Ser Gln	
440 445 450	
CTC AAT GAA AAT GAG ACT GAA ACA GCA CTG GAA AAA GGT ATA CAC ATT	2284
Leu Asn Glu Asn Glu Thr Glu Thr Ala Leu Glu Lys Gly Ile His Ile	
455 460 465 470	
TAT CCG AAT CCC TAT AAA AAC GGT CCA TTG ACA ATC GAT TTT GGC AAA	2332
Tyr Pro Asn Pro Tyr Lys Asn Gly Pro Leu Thr Ile Asp Phe Gly Lys	
475 480 485	
CCC TTC AGC GGC GAG GTC CAA ATC ACC GGT TTA AAC GGT AGA ACA TTC	2380
Pro Phe Ser Gly Glu Val Gln Ile Thr Gly Leu Asn Gly Arg Thr Phe	
490 495 500	
TTA AGA AGA AAT GTT GTC GAT CAA ACT TCG GTT CAG CTC CTA GAA TCC	2428
Leu Arg Arg Asn Val Val Asp Gln Thr Ser Val Gln Leu Leu Glu Ser	
505 510 515	
AAA TCT AAA TTC AAG AGC GGT CTA TAT ATC GTT AAA ATT AGT GGC CCG	2476
Lys Ser Lys Phe Lys Ser Gly Leu Tyr Ile Val Lys Ile Ser Gly Pro	
520 525 530	
GAT GGA GAG GTT TCA AAA AAG ATA CTC GTG GAG TAACTAAAAA TCAATTTTTA	2529
Asp Gly Glu Val Ser Lys Lys Ile Leu Val Glu	
535 540 545	
CAGGATTACA GACGGGCAAA GGGATTTTCC TTTGCCCGTT TTAAAAATTA TGGGCGGAAA	2589
CGATTGTTGC G	2600

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Lys Lys Pro Asn Phe Tyr Gly Lys Met Gly Arg Thr Ala Leu Ser	
1 5 10 15	
Ser Leu Phe Tyr Leu Phe Phe Leu Gly Leu Val Tyr Gly Gln Gln Pro	
20 25 30	

Thr	Lys	Thr	Ser	Asn	Pro	Asn	Asp	Gln	Trp	Thr	Ile	Lys	Trp	Ser	Ala	35	40	45
Ser	Asp	Glu	Phe	Asn	Lys	Asn	Asp	Pro	Asp	Trp	Ala	Lys	Trp	Ile	Lys	50	55	60
Thr	Gly	Asn	Leu	Pro	Asn	Thr	Ser	Ala	Trp	Lys	Trp	Asn	Asn	Gln	Lys	65	70	75
Asn	Val	Lys	Ile	Ser	Asn	Gly	Ile	Ala	Glu	Leu	Thr	Met	Arg	His	Asn	85	90	95
Ala	Asn	Asn	Thr	Pro	Pro	Asp	Gly	Gly	Thr	Tyr	Phe	Thr	Ser	Gly	Ile	100	105	110
Phe	Lys	Ser	Tyr	Gln	Lys	Phe	Thr	Tyr	Gly	Tyr	Phe	Glu	Ala	Lys	Ile	115	120	125
Gln	Gly	Ala	Asp	Ile	Gly	Glu	Gly	Val	Cys	Pro	Ser	Phe	Trp	Leu	Tyr	130	135	140
Ser	Asp	Phe	Asp	Tyr	Ser	Val	Ala	Asn	Gly	Glu	Thr	Val	Tyr	Ser	Glu	145	150	155
Ile	Asp	Val	Val	Glu	Leu	Gln	Gln	Phe	Asp	Trp	Tyr	Glu	Gly	His	Gln	165	170	175
Asp	Asp	Ile	Tyr	Asp	Met	Asp	Leu	Asn	Leu	His	Ala	Val	Val	Lys	Glu	180	185	190
Asn	Gly	Gln	Gly	Val	Trp	Lys	Arg	Pro	Lys	Met	Tyr	Pro	Gln	Glu	Gln	195	200	205
Leu	Asn	Lys	Trp	Arg	Ala	Met	Asp	Pro	Ser	Lys	Asp	Phe	His	Ile	Tyr	210	215	220
Gly	Cys	Glu	Val	Asn	Gln	Asn	Glu	Ile	Ile	Trp	Tyr	Val	Asp	Gly	Val	225	230	235
Glu	Val	Ala	Arg	Lys	Pro	Asn	Lys	Tyr	Trp	His	Arg	Pro	Met	Asn	Val	245	250	255
Thr	Leu	Ser	Leu	Gly	Leu	Arg	Lys	Pro	Phe	Val	Lys	Phe	Phe	Asp	Asn	260	265	270
Lys	Asn	Asn	Ala	Ile	Asn	Pro	Glu	Thr	Asp	Ala	Lys	Ala	Arg	Glu	Lys	275	280	285
Leu	Ser	Asp	Ile	Pro	Thr	Ser	Met	Tyr	Val	Asp	Tyr	Val	Arg	Val	Trp	290	295	300
Glu	Lys	Ser	Ala	Gly	Asn	Thr	Thr	Asn	Pro	Pro	Thr	Ser	Glu	Val	Gly	305	310	315
Thr	Leu	Lys	Thr	Lys	Gly	Ser	Lys	Leu	Val	Ile	Asp	His	Trp	Asp	Ala	325	330	335
Ser	Thr	Gly	Thr	Ile	Ser	Ala	Val	Ser	Asn	Asn	Thr	Lys	Thr	Gly	Gln	340	345	350
Tyr	Ala	Gly	Ser	Val	Asn	Asn	Ala	Ser	Ile	Ala	Gln	Ile	Val	Thr	Leu	355	360	365
Lys	Ala	Asn	Thr	Ser	Tyr	Lys	Val	Ser	Ala	Phe	Gly	Lys	Ala	Ser	Ser	370	375	380
Pro	Gly	Thr	Ser	Ala	Tyr	Leu	Gly	Ile	Ser	Lys	Ala	Ser	Asn	Asn	Glu	385	390	395
																		400

Leu	Ile	Ser	Asn	Phe	Glu	Phe	Lys	Thr	Thr	Ser	Tyr	Ser	Lys	Gly	Glu	
				405					410					415		
Ile	Glu	Ile	Arg	Thr	Gly	Asn	Val	Gln	Glu	Ser	Tyr	Arg	Ile	Trp	Tyr	
				420					425					430		
Trp	Ser	Ser	Gly	Gln	Ala	Tyr	Cys	Asp	Asp	Phe	Asn	Leu	Val	Glu	Ile	
				435					440					445		
Asn	Ser	Gly	Ala	Ser	Gln	Leu	Asn	Glu	Asn	Glu	Thr	Glu	Thr	Ala	Leu	
				450					455					460		
Glu	Lys	Gly	Ile	His	Ile	Tyr	Pro	Asn	Pro	Tyr	Lys	Asn	Gly	Pro	Leu	
465					470					475					480	
Thr	Ile	Asp	Phe	Gly	Lys	Pro	Phe	Ser	Gly	Glu	Val	Gln	Ile	Thr	Gly	
				485					490					495		
Leu	Asn	Gly	Arg	Thr	Phe	Leu	Arg	Arg	Asn	Val	Val	Asp	Gln	Thr	Ser	
				500					505					510		
Val	Gln	Leu	Leu	Glu	Ser	Lys	Ser	Lys	Phe	Lys	Ser	Gly	Leu	Tyr	Ile	
				515					520					525		
Val	Lys	Ile	Ser	Gly	Pro	Asp	Gly	Glu	Val	Ser	Lys	Lys	Ile	Leu	Val	
				530					535					540		
Glu																
545																